

C1

- (b) a nucleotide sequence consisting of SEQ ID NO:1;
- (c) a nucleotide sequence consisting of SEQ ID NO:3; and
- (d) a nucleotide sequence that is completely complementary over the entire length of a nucleotide sequence of (a)-(c).

C2

28.
claim #1

(Twice Amended) A vector comprising the nucleic acid molecule of

C3

24. (Amended) A process for producing a polypeptide comprising the amino acid sequence of SEQ ID NO:2, the process comprising culturing the host cell of claim 6 under conditions sufficient for the production of said polypeptide, and recovering said polypeptide, thereby producing said polypeptide.

In the Specification:

Please replace the two consecutive paragraphs beginning with the last paragraph on page 12 through the first full paragraph on page 13 of the specification with the following two consecutive paragraphs:

C4

The comparison of sequences and determination of percent identity and similarity between two sequences can be accomplished using a mathematical algorithm. (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data, Part 1*, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991). In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package, using either a Blossom 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a